

# Supapixel Segmentation for Endmember Detection in Hyperspectral Images

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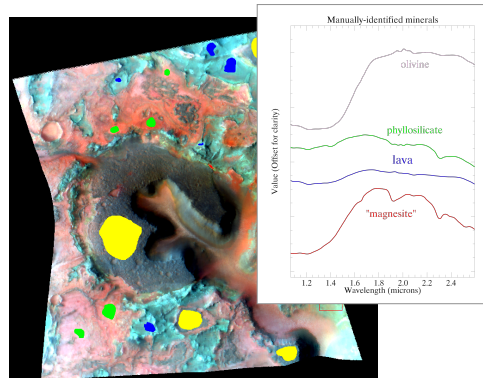
## Overview

"Supapixel segmentation" is a novel approach to facilitate statistical analyses of hyperspectral image data with high spatial resolution and subtle spectral features.

Supixels oversegment the image into homogeneous regions comprised of several contiguous pixels. This can improve signal strength by exploiting scene features' spatial contiguity: isolated spectral features are likely to be noise, but spectral features that appear in adjacent pixels are likely to indicate features in the scene. The mean spectra of each supixel comprise a noise-reduced dataset that improves endmember detection for the images in our study.

## Dataset

We evaluated the approach for several images from the Compact Reconnaissance Imaging Spectrometer (CRISM). We used the 1000-2500nm wavelengths of images frt00003e12, frt00008158, frt0000863e, and frt00003fb9. We cleaned the images with atmospheric correction based on Olympus Mons spectra (courtesy the Brown Crism Analysis Tool). We then preprocessed the data with a radius-1 median filter in the spectral domain.



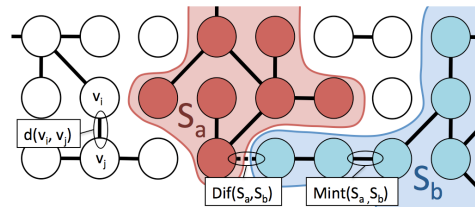
An analyst labeled each image with regions of interest corresponding to the 4-8 principal mineral types. According to the linear mixing assumption, each of the scene pixels' spectra are a linear combination of these "endmembers." Above: endmembers for CRISM image 3e12.



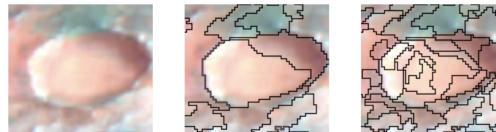
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## Segmentation Approach

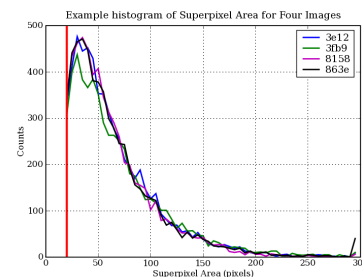
We generate superpixels with the Felzenszwalb/Huttenlocher graph-based segmentation. The goal is to shatter the image into thousands of superpixels, each with an area of approximately 20 image pixels. We represent the image as a graph of pixels with edge weights proportional to spectral difference (here, a Euclidean distance metric).



Above: Graph representation of pixels in a hyperspectral image. Left: an example edge  $(v_i, v_j)$  connects vertices  $v_i$  and  $v_j$ . Right: we consider joining segments  $S_a$  and  $S_b$ . We compare the maximum internal distance in their spanning trees  $Mint(S_a, S_b)$  with the minimum connecting distance  $Dif(S_a, S_b)$ . Here the candidate edge with minimum distance is denoted by a dashed line.



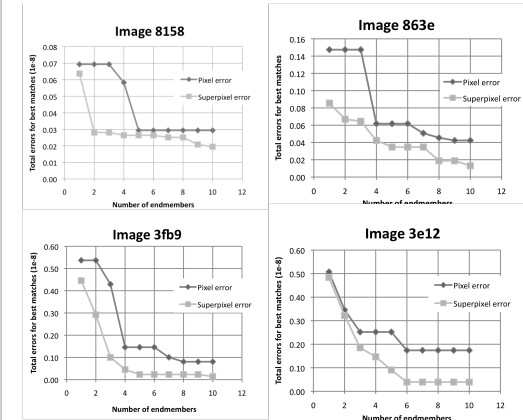
Above: Users can alter a "minimum size" parameter to control segments' resolution. Above we see a segmentation of an image patch from CRISM frt0000f3e12, Left: Original subimage. Center: coarse segmentation, minimum region size 100. Right: fine segmentation, minimum region size 20.



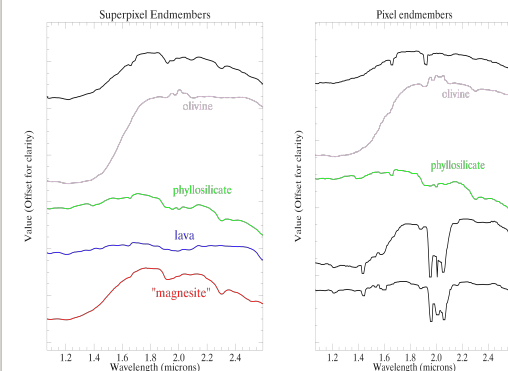
Above: Distribution of segment sizes for each of four images, here with a minimum size of 20 (red line).

## Endmember Detection

We presume a standard linear mixing model, and apply a Sequential Maximum Angle Convex Cone endmember extraction technique to automatically recover salient mineral classes.



Here we compare the results using superpixel and pixel-based representations. Performance scores are the total of squared errors over all wavelengths between each of the Analyst's "ground truth" spectra and its best match among the set of endmember spectra. Supapixel representations yield endmember spectra that are closer to the minerals of interest supplied by manual analysis.



Above: superpixel representations reduce noise and yield endmember spectra that better match the actual elements of the scene. Here we see the top five recovered endmembers for CRISM image 3e12 (compare to the ground truth minerals at far left).